

GenCore version 5.1.4\_p5\_4578  
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## OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 15, 2003, 15:07:49 ; Search time 74.0238 Seconds  
(without alignments)  
1537.035 Million cell updates/sec

Title: US-08-978-217-2

Perfect score: 1980  
Sequence: 1 MATCHESINFINESAMYS.....YKFGKNSGCKKEEVLQSHN 371

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 44162 segs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Command line parameters:

-MODE=frame\_p2n.model -DEV=x1p  
-Q=/cgn2\_1/USPTO.spool/US08978217/runat\_14032003\_141838\_13457/app\_query.fasta\_1.1500  
-DB=Issued Patents NA -OPMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi  
-LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTMT=pct -NGRAM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US08978217@cgn2\_1.1.131@runat\_14032003\_141838\_13457 -NCPU=6 -ICPU=3  
-NO XLPXY -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

## Database :

Issued Patents NA.\*  
1: /cgn2\_6/prodata/1/ina/5A.COMB.seq.\*  
2: /cgn2\_6/prodata/1/ina/5B.COMB.seq.\*  
3: /cgn2\_6/prodata/1/ina/6A.COMB.seq.\*  
4: /cgn2\_6/prodata/1/ina/6B.COMB.seq.\*  
5: /cgn2\_6/prodata/1/ina/PCTUS.COMB.seq.\*  
6: /cgn2\_6/prodata/1/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1980	100.0	1920	1	US-08-746-789A-1
2	559	28.2	5427	3	US-09-009-913-2
3	555.5	28.1	5510	3	US-09-009-913-3
4	555.5	28.1	5667	3	US-09-009-913-4
5	519.5	26.2	852	4	US-09-020-956-44
6	519.5	26.2	852	4	US-09-030-607-44
7	519.5	26.2	852	4	US-09-605-785-44
8	519.5	26.2	852	4	US-09-439-313-44
9	519.5	26.2	852	4	US-09-352-616A-44
10	519.5	26.2	852	4	US-09-232-149A-44
11	486.5	24.6	848	3	US-09-009-913-338
12	422	21.3	2280	3	US-09-009-913-8

13	422	21.3	2428	3	US-09-009-913-6	Sequence 6, Appl
14	422	21.3	2498	3	US-09-009-913-10	Sequence 10, Appl
15	246.5	12.4	2975	1	US-08-368-281-1	Sequence 1, Appl
16	242	12.2	3240	1	US-08-368-281-3	Sequence 3, Appl
17	238.5	12.0	1905	4	US-09-055-113-2	Sequence 2, Appl
18	234.5	11.8	1752	4	US-09-360-779-1	Sequence 1, Appl
19	234.5	11.8	1752	4	US-09-435-335-1	Sequence 1, Appl
20	233	11.8	1752	4	US-09-344-579-1	Sequence 1, Appl
21	228	11.5	1604	5	PCT-US83-06251-9	Sequence 43, Appl
22	228	11.5	1604	5	PCT-US83-06251-9	Sequence 9, Appl
23	213.5	10.8	1528	4	US-08-878-177-3	Sequence 3, Appl
24	212	10.7	2938	2	US-08-433-443B-3	Sequence 3, Appl
25	207	10.5	1447	4	US-08-878-177-1	Sequence 1, Appl
26	203.5	10.3	2266	2	US-09-213-767-1	Sequence 1, Appl
27	190	9.6	2410	2	US-08-780-835B-1	Sequence 1, Appl
28	190	9.6	2410	4	US-09-303-268-1	Sequence 1, Appl
29	190	9.6	2410	4	US-09-116-049-1	Sequence 1, Appl
30	189	9.5	2667	2	US-08-469-412A-1	Sequence 1, Appl
31	189	9.5	2667	4	US-09-021-715-1	Sequence 1, Appl
32	185.5	9.4	2064	4	US-08-875-944B-1	Sequence 1, Appl
33	185.5	9.4	2064	4	US-09-116-049-3	Sequence 3, Appl
34	158	8.0	1364	1	US-08-306-691B-50	Sequence 50, Appl
35	158	8.0	1364	5	PCT-US93-06251-65	Sequence 65, Appl
36	129	6.5	2544	2	US-08-469-412B-6	Sequence 6, Appl
37	129	6.5	2544	4	US-09-021-715-6	Sequence 6, Appl
38	109.5	5.5	1131	4	US-09-410-464-7	Sequence 7, Appl
39	109.5	5.5	1308	4	US-09-410-464-6	Sequence 6, Appl
40	101.5	5.1	3777	3	US-09-121-321-15	Sequence 15, Appl
41	101.5	5.1	3777	4	US-08-933-803A-15	Sequence 15, Appl
42	99.5	5.0	1640	3	US-09-330-095-2	Sequence 2, Appl
43	99	5.0	2516	1	US-07-914-282D-2	Sequence 2, Appl
44	99	5.0	2516	1	US-08-276-887A-2	Sequence 2, Appl
45	99	5.0	2516	5	PCT-US93-02460-2	Sequence 2, Appl

## ALIGNMENTS

RESULT 1  
US-08-746-789A-1  
; Sequence 1, Application US/08746789A  
; Patent No. 5789200  
; GENERAL INFORMATION:  
; APPLICANT: Ismail Kola, Martin J. Tynms, Christine DeBouck  
; TITLE OF INVENTION: A No. 5789200el Human ETS Family Member, ELP3  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road, P.O. Box 1539  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
; COMPUTER: IBM 486  
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS  
; SOFTWARE: MICROSOFT WORD  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/746, 789A  
; FILING DATE: No. 5789200el 15, 1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: William T. Han  
; REGISTRATION NUMBER: 34,344  
; REFERENCE/DOCKET NUMBER: ATG 50024  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610 270 5219  
; TELEFAX: 610 270 4026  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:

; LENGTH: 1920  
 ; TYPE: Nucleic Acid  
 ; STRANDEDNESS: Single  
 ; TOPOLOGY: Linear  
 ; ANTI-SENSE: No  
 ; US-08-746-789A-1

Alignment Scores:  
 Pred. No.: 3,676-186 Length: 1920  
 Score: 1980.00 Matches: 371  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 1 Gaps: 0

US-08-978-217-2 (1-371) x US-08-746-789A-1 (1-1920)

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 QY 21 SerGluaspserThrleuAlaserValProProAlaAlaThrPhaglyAlaaspleu 40  
 Db 175 TCGAGGACTCCACCTTGCTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 234  
 QY 41 ValleurThrleuSerAspProGlnmetSerleuGluGlyThrGlylyleAlaserTrpleu 60  
 Db 225 GTACTGACCTTGACGACCAACCCAGATGTCATTTGAGAGGTACAGAAAGCTGCTTG 294  
 QY 61 GlyGluGlnProGlnPheTrpSerlyThrGlnValleuAspTrpleSerTrpGlnVal 80  
 Db 295 GGGGAACAGCCCCAGCTTGTGTGAAAGCGCAGGTTCTGATCGATCGATCAACAGTG 354  
 QY 81 GluIyAsenlyuTyraAspAlaserAlaIleaspheserArgCysAspmetAspGlyAla 100  
 Db 355 GAGAGAAACAAATGACAGCAAGCCGATGACTTCTCGATGACATGATGAGGCGC 414  
 QY 101 ThrleuCyAsenCyAlaleuGluGluLeuValPheGlyProleuGlyAspGln 120  
 Db 415 ACCCTCTGCAATTTGCTTCCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 474  
 QY 121 LeuHilaIaGlnleuArgAspleuThrSerSerSerSerAspGluLeuSerTrpIlele 140  
 Db 475 CTCCATGCCACCTGAGACCTCACTTCCAGCTCTTGATGAGCTCAGTTGATCAT 534  
 QY 141 GluLeuLeuGluLyAspGlyMetAlaPheGlnGluAlaLeuAspProGlyProPheAsp 160  
 Db 535 GAGCTGCTGAGAAAGATGAGCTGCTTCCAGAGGCCCTAGACCAGGCGCTTTCAC 594  
 QY 161 GlnGlySerProPheAlaGlnGluLeuLeuAspGlyGlnGlnAlaSerProTyrlHis 180  
 Db 595 CAGGCGACGCCCTTTGCCAGAGCTGCTGAGACGAGCTCAGCAACGCCAGCCCTTAC 654  
 QY 181 ProGlySerCyGlyAlaGlyAlaProSerProGlySerSerAspValSerThrAlaGly 200  
 Db 655 CCCGCGAGCTGTGGCGACAGAGCCCTCCCTGGAGCTTCCAGCTCCACCGAGGG 714  
 QY 201 ThrGlyAlaSerArgSerSerHisSerSerAspSerGlyGlySerAspAlaPheLeuAsp 220  
 Db 715 ACTGTGTCTTTCGAGAGCTCCCACTCTCAGACTCGGTGGAAGTACCTGAGCTGGAT 774  
 QY 221 ProThrAspGlyLyLeuLeuPheProSerAspGlyPheArgAspCylylylyAspPro 240  
 Db 775 CCCACTGATGGCAAGCTTTCCCGACGATGGTTTTCGATGCTGCAAGAAAGGGGATCCC 834  
 QY 241 LyshIaGlyLyAspGlylyAspGlyArgProArgLyLeuSerlyGlylyTrpAspCys 260  
 Db 835 AAGCAACGGGAACGGGAACGAGGCGCGCCCGAAGACTAGCAAGAGTACTGGAGCTGT 894  
 QY 261 LeuGluGlyLylylylylylylyshIaIaProArgGlyThrHisleuTrpGluPheleArg 280  
 Db 895 CTGAGGGGCAAGAGAGCAAGCAAGCGCCAGAGGCAACCCACTGTGGAGATTTCATCCGG 954

QY 281 AspIleleuIleHisPProGluLeuAsnGluGlyLeuMetlystrpGluAsnArgHieGlu 300  
 Db 955 GACATCTCATCCACCGGAGCTCAACAGAGCCCTCATGAAATGGGGAATCCGCATGAA 1014  
 QY 301 GlyValPheLyPheleuArgSerGluAlaValIaGlnleuTrpGlyGlnlyleLylys 320  
 Db 1015 GCGCTTCAAGTTCCTGCGCTCCGAGCTGTGGCCCACTATGGGGCAAAAGAAAAG 1074  
 QY 321 AsnSerAsnMetThrTrpGlyLylyleuSerArgAlaMetArglyTrpTrpLyAspGlu 340  
 Db 1075 AACGCAACATGACTCTAGAGAACTGAGCGCGGCATGAGTACTACAAACGGGAG 1134  
 QY 341 IleleuGluArgValAspGlyArgArgleuValTrpLyPheGlyLyAsnSerSerGly 360  
 Db 1135 ATCTCGAAACGGGTGTGATGGCCGCGGACTCCTCTACAAAGTTGGCAAAACTCAAGCGGC 1194

QY 361 TrpLyGluGluGluValleuGlnSerArgAsn 371

Db 1195 TGAAGAGAGAAAGATTCTCCAGAGTCGGAAC 1227

RESULT 2

US-09-009-913-2

; Sequence 2, Application US/09009913

; Patent No. 6087485

; GENERAL INFORMATION:

; APPLICANT: Axis Pharmaceuticals, Inc.

; TITLE OF INVENTION: Asthma Related Genes

; NUMBER OF SEQUENCES: 339

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Bozicevic & Reed, LLP

; STREET: 285 Hamilton Ave, Suite 200

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/009,913

; FILING DATE: 21-JAN-1998

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Sherwood, Pamela J

; REGISTRATION NUMBER: 36,677

; REFERENCE/DOCKET NUMBER: SEQ-4P

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-327-3231

; TELEFAX: 650-327-3231

; TELEX:

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 5427 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: CDNA

; US-09-009-913-2

Alignment Scores:

Pred. No.: 4,586-45 Length: 5427

Score: 559.00 Matches: 140

Percent Similarity: 47.42% Conservative: 44

Best Local Similarity: 36.08% Mismatches: 88

Query Match: 28.23% Indels: 116

DB: 3 Gaps: 12

US-08-978-217-2 (1-371) x US-09-009-913-2 (1-5427)



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Db 536 CAGCTCCCTTACAGCAACTTGCAGCATCTGAAAGTGAACGGCCAGCGAGTGTGAC--- 592
QY 136 LeuSerTripleIleGluLeuLeuGluLysApsGlyMetAlaPheGlnGluAlaLeuAps 155
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 593 -----CTGTTCCAGTCC----- 604
QY 156 ProGlyProPheApsGlnGlySerProPheAlaGlnGluLeuLeuApsApsGlyGlnGln 175
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 605 -----ACACACAAATGCTATTCTCAAGACTGAACAA 634
QY 176 AlaSerProTyH1aPProGlySerCySglYalAglYalAProSerProGlySerSerAps 195
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 635 ACTGAGCCT----- 643
QY 196 ValSerThrAlaGlyThrcGlyAlaSerAArgSerSerHisSerSerSerApsGlySer 215
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 644 ---TCCATCATGACACCTGGAAGACGAAAGCATATTATTATGACACCAACTATGCTAGC 700
QY 216 AapValApsLeuApsProThrApsGlyLysLeuPhePheProSerApsGlyPheAArgApsCys 235
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Db 701 ACAGTAGATTG-----TTGGACAGCAAAACTTTC-----TGC 733
QY 236 LysLys-----GlyApsProLysHisGly 243
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 734 CGGGCTCATGCTCCATGACAAACACACACACTGACCTTCCTTGGACAGACCTGATATG 793
QY 244 LysAArgLysAArgGlyAArgProAArgLysLysSerLysGlyTrpApsCySleuGluGly 263
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 794 AAAAAAGACCAAGACCCCTGCAAGTCCACACCCAAA----- 832
QY 264 LysLysSerLysHisAArgAProAArgGlyThrcHisLeuTrpGluPheIleAArgApsIleLeu 283
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Db 833 -----AAGGACAAACCCGAGAGGGAGCTCACTTATGGAAATTCATCCGCGACATCTTC 883
QY 284 IleHisProGlnLeuApsnGlnGlyLysMetLysTrpGluAAsnAArgHisGlnGlyAlaPhe 303
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 884 TTGAACCCGACACAGAACCCAGGATTTATTAATATGGGAAGACCGACTGAGGCGCTTC 943
QY 304 LysPheLeuAArgSerGlnAlaValAlaGlnLeuTrpGlyGlnLysLysLysApsnSerAps 323
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 944 AGGTTCTTGAATTCAGAGGAGCAGTGGCTCAGCTATGCGGTAAAAAGAAACAACACACAC 1003
QY 324 MetThrTyGlnLysLeuSerAArgAlaMetAArgTyTrpTyLysAArgGlnIleLeuGln 343
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Db 1004 ATGACCTATGAAGAGCTCAGCGAGCTATGAGTATTACTTACAAAAGAAATACAGAG 1063
QY 344 ArgValApsGlyAArgAArgLeuValTyTrpLysPheGlyLysApsnSerSerGlyTrpLysGln 363
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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QY 364 GluGlu 365
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Db 1124 AATGAA 1129

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/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/009,913
/ FILING DATE: 21-JAN-1998
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sherwood, Pamela J
/ REGISTRATION NUMBER: 36,677
/ REFERENCE/DOCKET NUMBER: SEQ-4P
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-327-3231
/ TELEFAX: 650-327-3231
/
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 5667 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/
/ US-09-009-913-4
/
/ Alignment Scores:
/ Pred. No.: 1.08e-44 Length: 5667
/ Score: 555.50 Matches: 126
/ Percent Similarity: 51.24% Conservative: 39
/ Best Local Similarity: 39.13% Mismatches: 78
/ Query Match: 28.06% Indels: 79
/ DB: 3 Gaps: 8
/
/ US-08-978-217-2 (1-371) x US-09-009-913-4 (1-5667)
QY 59 TrpLeuGlyGlnGlnProGlnPheTrpSerLysThrcGlnValLeuApsTrpIleSerTy 78
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 513 TGGCATGAATTCATCTCTCAGTACGACCAAGTACCAAGTGTGGAGATGCTCCAGCAC 572
QY 79 GlnValGluLysAAsnLysTyTrpApsAlaIleApsPheSerAArgCySapsMetAps 98
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 573 CTCCTGACACCAACACAGCTGATGCCAATTGTATCTCCATCAAGATTCGACATCAAC 632
QY 99 GlyAlaThrLeuCySapsCysAlaLeuGlnGluLeuAArgLeuValPheGlyProLeuGly 118
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 633 GGGGAGCACCTCTTGCAGCATGAGTTTGCAGAGTTCCACCCGGGCGGACGCGGGGG 692
QY 119 AergInLeuH1aGlnLeuAArgApleuThr-----SerSerSerSerApsglu 135
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 693 CAGCTCCCTTACAGCAACTTGCAGCATCTGAAAGTGAACGGCCATGCAAGTGTGAC--- 749
QY 136 LeuSerTripleIleGluLeuLeuGluLysApsGlyMetAlaPheGlnGluAlaLeuAps 155
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 750 -----CTGTTCCAGTCC----- 761
QY 156 ProGlyProPheApsGlnGlySerProPheAlaGlnGluLeuLeuApsApsGlyGlnGln 175
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 762 -----ACACACAAATGCTATTGTCAGACTGAACAA 791
QY 176 AlaSerProTyH1aPProGlySerCySglYalAglYalAProSerProGlySerSerAps 195
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 792 ACTGAGCCT----- 800
QY 196 ValSerThrAlaGlyThrcGlyAlaSerAArgSerSerHisSerSerSerApsGlySer 215
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 801 ---TCCATCATGACACCTGGAAGACGAAAGCATTTATATGACACCAACTATGCTAGC 857
QY 216 AapValApsLeuApsProThrApsGlyLysLeuPhePheProSerApsGlyPheAArgApsCys 235
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 858 ACAGTAGATTG-----TTGGACAGCAAAACTTTC-----TGC 890

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```

RESULT 4
US-09-009-913-4
/ Sequence 4, Application US/09009913
/ Patent No. 6087485
/ GENERAL INFORMATION:
/ APPLICANT: AYS Pharmaceuticals, Inc.
/ TITLE OF INVENTION: Asthma Related Genes
/ NUMBER OF SEQUENCES: 339
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Bozicevic & Reed, LLP
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94301
/ COMPUTER READABLE FORM:

```



Qy 356 LysAenSerSerGlyTrrpLysGluGlu 365  
 Db 142 AAGAATGCCGAGATGAGAGAAATGAA 113

RESULT 6  
 US-09-030-607-44/C  
 ; Sequence 44, Application US/09030607  
 ; Patent No. 6262245  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xu, Jiangchun  
 ; APPLICANT: Dillon, Davin C.  
 ; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO  
 ; NUMBER OF SEQUENCES: 224  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SEED and BERRY LLP  
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue  
 ; CITY: Seattle  
 ; STATE: WA  
 ; COUNTRY: USA  
 ; ZIP: 98104  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/030,607  
 ; FILING DATE: 25-FEB-1998  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Makl, David J.  
 ; REGISTRATION NUMBER: 31,392  
 ; REFERENCE/DOCKET NUMBER: 210121.427C3  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (206) 622-4900  
 ; TELEFAX: (206) 682-6031  
 ; INFORMATION FOR SEQ ID NO: 44:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 852 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Homo sapiens  
 ; US-09-030-607-44

Alignment Scores:  
 Pred. No.: 2,296-42 Length: 852  
 Score: 519.50 Matches: 121  
 Percent Similarity: 50.97% Conservative: 37  
 Best Local Similarity: 39.03% Mismatches: 73  
 Query Match: 26.24% Indels: 79  
 DB: 4 Gaps: 8

US-08-978-217-2 (1-371) x US-09-030-607-44 (1-852)

Qy 71 GlnValLeuAspTrrpLysGluValGluValAspLysTyrAspLysAlaIle 90  
 Db 850 CAGGTGTGGAGTGGTTCATCATCTCTGGACACCAACAGTGGATCTGTTATTC 791

Qy 91 AspPheSerArgCysAspMetAspGlyAlaThrLeuCysAsnCysAlaLeuGluGluLeu 110  
 Db 790 CCTTTCAGAGATGTGACATCAACGCGACGACCTTTGACAGCATGATTTGACGAGGTTG 731

Qy 111 ArgLeuValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThr 129  
 Db 730 ACCCGGCGCGACGAGCGCGGCGGCGANCTCTCTACAGCAACTTGACGATCTGAAGTGG 671

Qy 130 -----SerSerSerSerArgGlyLeuSerTrrpLysIleIleGluLeuLeuGluLysAspGly 147  
 Db 670 AACGGCCAGTGCAGTAGTGAC----- 650

Qy 148 MetAlaPheGlnGluAlaLeuAspProGlyProPheAspGlnGlySerProPheAlaGln 167  
 Db 649 ---CTGTTCCAGTCC-----ACACAC 632

Qy 168 GluLeuLeuAspAspGlyGlnGlnAlaSerProTrrpHisProGlySerCysGlyAlaGly 187  
 Db 631 AATGTCATTGTCACAGCTGAACTGAAGTGAAGCTT----- 599

Qy 188 AlaProSerProGlySerSerAspValSerThrAlaGlyThrGlyAlaSerArgSerSer 207  
 Db 598 -----TCCATCATGAACACTGTGAAAGACAGAACTAT 566

Qy 208 HisSerSerAspSerGlyGlySerAspValAspLeuAspProTrrpHisAspGlyLysLeuPhe 227  
 Db 565 TTATATGACACCACTATGTAACAGTGAATTTG-----TTGACAGCAAAACTTTG 512

Qy 228 ProSerAspGlyPheArgAspCysValLys----- 237  
 Db 511 -----TCCGGGCTCAGATCTCCATGACCAACCACTACCTT 473

Qy 238 -----GlyAspProLysHisGlyLysArgLysArgGlyArgProArgLysLeuSerLys 255  
 Db 472 CCTGTGACAGAGTCACTGATATGAAAAGAGCAAGACCCCTGCGCAAGTCCACAC 413

Qy 256 GlyTyrTrrpAspCysLeuGluGlyLysLysSerLysHisAlaProArgGlyThrHisLeu 275  
 Db 412 AAA-----AAGCAACACCCAGAGGGGCTCCTACTTA 383

Qy 276 TrrpLysPheIleArgAspLysLeuLeuHisProGlyLeuAsnGluGlyLeuMetLysTrrp 295  
 Db 382 TGGGAAATTCATCCGGACATCTCTTGAAACCAAGCAAGAACCCGAGTTATATAAATGG 323

Qy 296 GluAsnArgHisGluGlyValPheLysPheLeuArgSerGlyAlaValAlaGlnLeuTrrp 315  
 Db 322 GAAAGCCATCTGAGGGGCTTCAAGTTCTGAAATCAGAGGCGAGTGCCTACGATATGG 263

Qy 316 GlyGlnLysLysLysAsnSerAsnMetThrTyrGlyLysLeuSerArgAlaMetArgTyr 335  
 Db 262 GGTAAAAAGAACACACAGCGCATGACTATGAAAAAGCTCAGCGGCTATGAGATAT 203

Qy 336 TyrTrrpLysArgGluIleLeuGlnLysValAspGlyArgAspLeuValTrrpLysPheGly 355  
 Db 202 TACTACAAAAGAAATTCGTGAGCGTGTGATGACGAAAGCTGTATATAAATTTGGG 143

Qy 356 LysAenSerSerGlyTrrpLysGluGlu 365  
 Db 142 AAGAATGCCGAGATGAGAGAAATGAA 113

RESULT 7  
 US-09-605-785-44/C  
 ; Sequence 44, Application US/09605785  
 ; Patent No. 6321716  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xu, Jiangchun  
 ; APPLICANT: Dillon, Davin C.  
 ; APPLICANT: Mitcham, Jennifer L.  
 ; APPLICANT: Harlocker, Susan L.  
 ; APPLICANT: Jiang, Yugu  
 ; APPLICANT: Henderson, Robert A.  
 ; APPLICANT: Kalos, Michael D.  
 ; APPLICANT: Fanger, Gary R.  
 ; APPLICANT: Retter, Marc W.  
 ; APPLICANT: Stolk, John A.  
 ; APPLICANT: Day, Craig H.  
 ; APPLICANT: Vedrick, Thomas S.  
 ; APPLICANT: Carter, Derrick  
 ; APPLICANT: Li, Samuel  
 ; APPLICANT: Wang, Aijun  
 ; APPLICANT: Skeiky, Yasir A.W.  
 ; APPLICANT: Hepler, William  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
 ; FILE REFERENCE: 210121.427C16

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CURRENT APPLICATION NUMBER: US/09/605,785
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 44
LENGTH: 852
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(852)
OTHER INFORMATION: n = A,T,C or G
US-09-605-785-44

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## Alignment Scores:

Pred. No.:	2,29e-42	Length:	852
Score:	519.50	Matches:	121
Percent Similarity:	50.97%	Conservative:	37
Best Local Similarity:	39.03%	Mismatches:	73
Query Match:	26.24%	Indels:	79
DB:	4	Gaps:	8

US-08-978-217-2 (1-371) x US-09-605-785-44 (1-852)

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Qy 71 GlnValLeuAspTrpLleSerTyrGlnValGlnLysAsnLysTyrAspAlaSerAlaIle 90
    |||||  :::::  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 850 CAGGTGGAGAGTGGCTCCATCCCTCGACACCAACCGATGATGCAATTTGATC 791
Qy 91 AspheSerArgCysAspMetAspGlyAlaThrLeuCyAsnCySalAlaLeuGluLeu 110
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 790 CTTTCCANGAGTTGCATCAACGCGAGACCTTTGCACAGATGAGTTGCAGAGTTC 731
Qy 111 ArgLeuValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThr--- 129
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 730 ACCCGGGCGGAGGAGCGGGGCANCTCTCTACACCACTTGACACATCTGAAGTG 671
Qy 130 -----SerSerSerSerAspGluLeuSerTrpIleIleGluLeuGluLysAspGly 147
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 670 AACGCCAGTGCAGTAGTGAC----- 650
Qy 148 MetAlaPheGlnGlnAlaLeuAspProGlyProPheAspGlnGlySerProPheAlaGln 167
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 649 ---CTGTTCCAGTCC-----ACACAC 632
Qy 168 GluLeuLeuAspAspGlyGlnGlnAlaSerProTyrHisProGlySerCyGlyAlaGly 187
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 631 AATGTCATTGCAAGACTGAACAACTGAGCTT----- 599
Qy 188 AlaProSerProGlySerSerAspValSerThrAlaGlyThrGlyAlaSerArgSerSer 207
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 598 -----TCCATCATGAACACCTGGAAGACNAGACTAT 566
Qy 208 HisSerSerAspSerGlyGlySerAspValAspLeuAspProThrAspGlyLysLeuPhe 227
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 565 TTATATGACACCACTATGATGACACAGTAGATTG-----TTGACACGACAAACTTTC 512
Qy 228 ProSerAspGlyPheAspAspCysLysLys----- 237
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 511 -----TGCCTGGGCTCAGATTCCTCATGACACCAACCACTGACCTT 473
Qy 238 -----GlyAspProLysHisGlyLysArgLysArgGlyAspProArgLysLeuSerLys 255
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 472 CCGTTCGACAGTCACTGATATGAAAAAGACGACAGCCCCCTGCCAATGCCACACC 413
Qy 256 GluTyrTrpAspCysLeuGlnGlyLysLysSerLysHisAlaProArgGlyThrHisLeu 275
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 412 AAA-----AAGCAACACCGAGAGGAGCTCCTCACTTA 383
Qy 276 TrpGluPheIleArgAspIleLeuIleHisProGluLeuAsnGlnGlyLeuMetLysTrp 295
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 382 TGGGAATTCATCCCGACATCTCTTGAACCAAGCAAGAACCAAGGATTATATAAATGG 323
Qy 296 GluAsnArgHisGlnGlyValPheLysPheLeuArgSerGlnAlaValAlaGlnLeuTrp 315

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Db 322 GAAGACCGATCTAGGGCGCTTCAAGTTCTTGAATCAAGGAGGAGTGGCTCAGCTATGG 263
Qy 316 GlyGlnLysLysLysAsnSerAspMetThrTyrGlnLysLeuSerArgAlaMetArgTyr 335
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 262 GGTAAAGAAAGAAACAACACACAGCATGACCTATGAAAGCTCAGCCGACGATATAGATAT 203
Qy 336 TyrTrpLysArgGluIleLeuGlnValArgValAspGlyArgLeuValTyrLysPheGly 355
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 202 TACTACAAAGAGAAATTTCTGAGCGGTGTGATGACGAAAGACTGTATATTAATTGGG 143
Qy 356 LysAsnSerSerGlyTrpLysGluGlu 365
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 142 AAGAATGCCCGAGATGAGAGAAATGAA 113

```

## RESULT 8

US-09-439-313-44/C

```

Sequence 44, Application US/09439313
Patent No. 6329505
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitchem, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yugu
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439, 313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 44
LENGTH: 852
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(852)
OTHER INFORMATION: n = A,T,C or G
US-09-439-313-44

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## Alignment Scores:

Pred. No.:	2,29e-42	Length:	852
Score:	519.50	Matches:	121
Percent Similarity:	50.97%	Conservative:	37
Best Local Similarity:	39.03%	Mismatches:	73
Query Match:	26.24%	Indels:	79
DB:	4	Gaps:	8

US-08-978-217-2 (1-371) x US-09-439-313-44 (1-852)

```

Qy 71 GlnValLeuAspTrpLleSerTyrGlnValGlnLysAsnLysTyrAspAlaSerAlaIle 90
    |||||  :::::  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 850 CAGGTGGAGAGTGGCTCCATCCCTCGACACCAACCGATGATGCAATTTGATC 791
Qy 91 AspheSerArgCysAspMetAspGlyAlaThrLeuCyAsnCySalAlaLeuGluLeu 110
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 790 CTTTCCANGAGTTGCATCAACGCGAGACCTTTGCACAGATGAGTTGCAGAGTTC 731
Qy 111 ArgLeuValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThr--- 129
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 730 ACCCGGGCGGAGGAGCGGGGCANCTCTCTACACCACTTGACACATCTGAAGTG 671
Qy 130 -----SerSerSerSerAspGluLeuSerTrpIleIleGluLeuGluLysAspGly 147
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 670 AACGCCAGTGCAGTAGTGAC----- 650

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```

Qy 148 MetAlaPheGlnGluAlaLeuAspProGlyProPheAspGlnGlySerProPheAlaGln 167
Db 649 ---CTGTTCCAGTCC-----ACACAC 632
Qy 168 GluLeuLeuAspAspGlyGlnGlnAlaSerProTyrHisProGlySerCysGlyAlaGly 187
Db 631 AATGTCATTGTCAGACTGACAGCAACTGAGCTT----- 599
Qy 188 AlaProSerProGlySerSerAspValSerThrAlaGlyThrGlyValaSerArgSerSer 207
Db 598 -----TCCATCATGAAACCTTGAAACACAGAACTAT 566
Qy 208 HisSerSerAspSerGlyGlySerAspValAspLeuAspProThrAspGlyTyrLeuPhe 227
Db 565 TTATATGACACCACTATGATGACAGATGATTTG-----TTGAGACAGCAAACTTTC 512
Qy 228 ProSerAspGlyPheArgAspCysLeuValys----- 237
Db 511 -----TGCCGGGCTCAGATCTCCATGACAACCACTGACCTT 473
Qy 238 -----GlyAspProLysHisGlyLysArgLysArgGlyArgProArgLysLeuSerLys 255
Db 472 CCTGTTGCAGAGTCACTGATATGAAAGAGCAAGACCCCTGCGCAAGTCCACACACC 413
Qy 256 GluTyrTyrPheAspCysLeuGlnGlyLysLysSerLysHisAlaProArgGlyTyrHisLeu 275
Db 412 AAA-----AAGCAACAACCGAGAGGACTCCTTA 383
Qy 276 TrpGluPheIleArgAspIleLeuIleHisProGluLeuAspGlnGlyLeuMetLysTrp 295
Db 382 TGGGAATTCATCCGGGACATCTCTTGAACCCAGACAAACCCAGGATTAATAAATGG 323
Qy 296 GluAsnArgHisGlnGlyValPheLysPheLeuArgSerGluAlaValAlaGlnLeuTrp 315
Db 322 GAAGCCCATCTGAGGGGCTCTTCAAGTTCTTGAATCAGAGGAGCTGACTATAG 263
Qy 316 GlnGlnLysLysLysAsnSerAsnMetThrTyrGlnLysLeuSerArgAlaMetArgTyr 335
Db 262 GGTAAAAAGAAAGAACACAGCAGCATGACCTATGAAAGACTCAGCGAGCTATGAGATAT 203
Qy 336 TyrTyrLysArgGluIleLeuGlnLysValAspGlyArgArgLeuValTyrLysPheGly 355
Db 202 TACTCAAAAGAAATTCGTGAGCGGTGTGATGACGAAGACTGGTATATTAATTTGGG 143
Qy 356 LysAsnSerSerGlyTyrLysGlnGluGln 365
Db 142 AAGAAATGCCCGAGATGGAGAGAAATGAA 113

RESULT 9
US-09-352-616A-44/c
: Sequence 44, Application US/09352616A
: Patent No. 6195278
: GENERAL INFORMATION:
: APPLICANT: Dillon, Davin C.
: APPLICANT: Harlocker, Susan Louise
: APPLICANT: Jiang, Yugu
: APPLICANT: Xu, Jiangchun
: APPLICANT: Mitchem, Jennifer Lynn
: TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
: FILE REFERENCE: 210121.427C8
: CURRENT APPLICATION NUMBER: US/09/352,616A
: CURRENT FILING DATE: 1998-07-13
: NUMBER OF SEQ ID NOS: 472
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 44
: LENGTH: 852
: TYPE: DNA
: ORGANISM: Homo sapien
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(852)

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: OTHER INFORMATION: n = A,T,C or G
US-09-352-616A-44
Alignment Scores:
Pred. No.: 2,29e-42 Length: 852
Score: 519.50 Matches: 121
Percent Similarity: 50.97% Conservative: 37
Best Local Similarity: 39.03% Mismatches: 73
Query Match: 26.24% Indels: 79
DB: 4 Gaps: 8

US-08-978-217-2 (1-371) x US-09-352-616A-44 (1-852)
Qy 71 GlnValLeuAspTrpIleSerTyrGlnValGluLysAsnLysTyrAspAlaSerAlaIle 90
Db 850 CAGGTGTGAGATGGCTCCATCACTCCTTGACACCAACCACTGATGACATATGATATC 791
Qy 91 AspPheSerArgCysAspMetAspGlyAlaThrLeuCysAsnGlyAlaLeuGlnGluLeu 110
Db 790 CCTTTCANAGATTCTGACATCAACCGCGAGCACTTTGACAGATGATTTCCAGAGATTTC 731
Qy 111 ArgLeuValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThr--- 129
Db 730 ACCCGGGCGGCGAGGACGGCGGGGCGGAGCTCTCTACAGCAACTTGACACATCTGAAGTGG 671
Qy 130 -----SerSerSerSerAspGluLeuSerTrpIleIleGluLeuGluLysAspGly 147
Db 670 AACGGCCAGTGCAGATGATGAC----- 650
Qy 148 MetAlaPheGlnGlnAlaLeuAspProGlyProPheAspGlnGlySerProPheAlaGln 167
Db 649 ---CTGTTCCAGTCC-----ACACAC 632
Qy 168 GluLeuLeuAspAspGlyGlnGlnAlaSerProTyrHisProGlySerCysGlyAlaGly 187
Db 631 AATGTCATTGTCAGACTGACAGCAACTGAGCTT----- 599
Qy 188 AlaProSerProGlySerSerAspValSerThrAlaGlyThrGlyValaSerArgSerSer 207
Db 598 -----TCCATCATGAAACCTTGAAACACAGAACTAT 566
Qy 208 HisSerSerAspSerGlyGlySerAspValAspLeuAspProThrAspGlyLysLeuPhe 227
Db 565 TTATATGACACCACTATGATGACAGATGATTTG-----TTGAGACAGCAAACTTTC 512
Qy 228 ProSerAspGlyPheArgAspCysLeuValys----- 237
Db 511 -----TGCCGGGCTCAGATCTCCATGACAACCACTGACCTT 473
Qy 238 -----GlyAspProLysHisGlyLysArgLysArgGlyArgProArgLysLeuSerLys 255
Db 472 CCTGTTGCAGAGTCACTGATATGAAAGAGCAAGACCCCTGCGCAAGTCCACACACC 413
Qy 256 GluTyrTyrPheAspCysLeuGlnGlyLysLysSerLysHisAlaProArgGlyTyrHisLeu 275
Db 412 AAA-----AAGCAACAACCGAGAGGACTCCTTA 383
Qy 276 TrpGluPheIleArgAspIleLeuIleHisProGluLeuAspGlnGlyLeuMetLysTrp 295
Db 382 TGGGAATTCATCCGGGACATCTCTTGAACCCAGACAAACCCAGGATTAATAAATGG 323
Qy 296 GluAsnArgHisGlnGlyValPheLysPheLeuArgSerGluAlaValAlaGlnLeuTrp 315
Db 322 GAAGCCCATCTGAGGGGCTCTTCAAGTTCTTGAATCAGAGGAGCTGACTATAG 263
Qy 316 GlnGlnLysLysLysAsnSerAsnMetThrTyrGlnLysLeuSerArgAlaMetArgTyr 335
Db 262 GGTAAAAAGAAAGAACACAGCAGCATGACCTATGAAAGCTCAGCGAGCTATGAGATAT 203
Qy 336 TyrTyrLysArgGluIleLeuGlnLysValAspGlyArgArgLeuValTyrLysPheGly 355
Db 202 TACTCAAAAGAAATTCGTGAGCGGTGTGATGACGAAGACTGGTATATTAATTTGGG 143

```



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Qy 356 LysAsnSerSerGlyTyrPlyGluGlu 365
Db 142 AAGAAATGCCGAGATGAGAGAAAATGAA 113

RESULT 10
US-09-232-149A-44/C
; Sequence 44, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 852
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) ... (852)
; OTHER INFORMATION: n = A,T,C or G
US-09-232-149A-44

Alignment Scores:
Pred. No.: 2,29e-42 Length: 852
Score: 519.50 Matches: 121
Percent Similarity: 50.97% Conservative: 37
Best Local Similarity: 39.03% Mismatches: 73
Query Match: 26.24% Indels: 79
DB: Gaps: 8

US-08-978-217-2 (1-371) x US-09-232-149A-44 (1-852)
Qy 71 GlnValLeuAspTrpIleSerTyrGlnValGluLysAsnLysTyrAspAlaSerAlaIle 90
Db 850 CAGGTGGGAGTGAGTGCATCACCCTCTGACACCAACGAGTGCATTTGATTC 791
Qy 91 AspPheSerArgCysAspMetAspGlyValThrLeuCysAsnCysAlaLeuGluLys 110
Db 790 CTTTCCANGAGTTGCAATCAACGCGACGACCTTTGACAGATGAGTTTGCAGAGTTC 731
Qy 111 ArgLeuValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThr--- 129
Db 730 ACCGGGGCGGAGGAGCGCGGGCANCTCCTCTACAGCACTTGACACATCTGAAGTGG 671
Qy 130 -----SerSerSerSerAspGluLeuSerTrpIleIleGluLeuGluLysAspGly 147
Db 670 AACGGCCAGTGCAGTAGTGCAC----- 650
Qy 148 MetAlaPheGlnGlnAlaLeuAspProGlyProPheAspGlnGlySerProPheAlaGln 167
Db 649 ---CTGTTCCAGTCC-----ACACAC 632
Qy 168 GluLeuLeuAspAspGlyGlnGlnAlaSerProTyrHisProGlySerCysGlyValaGly 187
Db 631 AATGTCATGTCAGACGACGAACTGAGCT----- 599
Qy 188 AlaProSerProGlySerSerAspValSerThrAlaGlyThrGlyAlaSerArgSerSer 207
Db 598 -----TCCATCATGAACACCTCGAAGACAGACAGACATAT 566
Qy 208 HisSerSerAspSerGlyGlySerAspValAspLeuAspProThrAspGlyLysLeuPhe 227
Db 565 TTATATGACACCAACTATGATGACAGATGTTG-----TTGACACGCAAACTTTC 512
Qy 228 ProSerAspGlyPheArgAspCysLysLys----- 237

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Db 511 -----TGCCGGGCTCAGATCTCCATGACACACACAGTACCTT 473
Qy 238 -----GlyAspProLysHisGlyLysArgLysArgGlyLysArgProArgLysLeuSerLys 255
Db 472 CCGTTGACAGATCACCCTGATATGAAAAAGAGCAAGACCCCTGCGCAAGTGCACACC 413
Qy 256 GluTyrTrpAspCysLeuGluGlyLysLysSerLysHisAlaProAlaGlyThrHisLeu 275
Db 412 AAA-----AAGCACAACCCGAGAGGAGTACCTTA 383
Qy 276 TrpGluPheIleArgAspIleLeuIleHisProGluLeuAsnGluGlyLysMetLysTrp 295
Db 382 TGGGAATTCATCCGCGACATCTTTAACCACAGAACCCAGGATTAATAAATGG 323
Qy 296 GluAsnArgHisGluGlyValPheLysPheLeuArgSerGlnAlaValAlaGlnLeuTrp 315
Db 322 GAAGACCGATCTAGGGCGCTTCAGGTTCTTGAAATCAGAGGAGTGGCTCAGCTATGG 263
Qy 316 GlyGlnLysLysLysAsnSerAsnMetThrTyrGlnLysLeuSerArgAlaMetArgTyr 335
Db 262 GTTAAAAAGAAACACACACAGCATGACCTATGAAAAAGCTCAGCCGACGCTATGATAT 203
Qy 336 TyrTyrLysArgGluIleLeuGluArgValAspGlyLysArgLeuValTyrLysPheGly 355
Db 202 TACTACAAAAGAGAAATTCGAGCGTGTGATGACGAAAGACTGTATTAATTTGGG 143
Qy 356 LysAsnSerSerGlyTyrPlyGluGlu 365
Db 142 AAGAAATGCCGAGATGAGAGAAAATGAA 113

RESULT 11
US-09-009-913-338
; Sequence 338, Application US/09009913
; Patent No. 6087485
; GENERAL INFORMATION:
; APPLICANT: Axy's Pharmaceuticals, Inc.
; TITLE OF INVENTION: Asthma Related Genes
; NUMBER OF SEQUENCES: 339
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bozicevic & Reed, LLP
; STREET: 285 Hamilton Ave, Suite 200
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: IBM Compatible
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,913
; FILING DATE: 21-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela J
; REGISTRATION NUMBER: 36,677
; REFERENCE/DOCKET NUMBER: SEQ-4P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-327-3231
; TELEFAX: 650-327-3231
; TELEX:
; INFORMATION FOR SEQ ID NO: 338:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 848 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:

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NAME/KEY: Coding Sequence
LOCATION: 1...848
OTHER INFORMATION:
US-09-009-913-338

Alignment Scores:
Pred. No.: 4.15e-39      Length: 848
Score: 486.50           Matches: 109
Percent Similarity: 51.53%      Conservative: 43
Best Local Similarity: 36.95%    Mismatches: 88
Query Match: 24.57%           Indels: 55
DB: 3                     Gaps: 5

US-08-978-217-2 (1-371) x US-09-009-913-338 (1-848)

QY 57 AAsERTpLeuGluGluInProGlnPheTyrSerLyThrGlnValLeuAspTrpIle 76
DB 118 ACCCAGTGGCAGTAAATCCACCTCAGTACTGAGCCAAATACAGGTGGGAATGGCTG 177
QY 77 SERTYGLNValGluYAsnLySTYrAspAlaSerAlaIleAspPheSerArgCysAsp 96
DB 178 CAGCACCTCTGGACCAACCAAGCAGTACGCTGAGTCCCTTCCAGAGATTCGAC 237
QY 97 MetAspGlyAlaThrLeuCYsAsnCysAlaLeuGluGluLeuArgValPheGlyPro 116
DB 238 ATTACGGGAGAACACCTGTGACAGTACGAGTTCACGAGGCGAGAGGCTCA 297
QY 117 LeuGlyAspGluLeuHisAlaGlnLeuArgAspLeuThr-----SerSerSer 133
DB 298 GCTGGCAGACTCTCTACACCACTTCAAGCATCTCAAGTGAAACGGCAATGCAAGT 357
QY 134 AspGluLeuSerTrpIleIleGluLeuGluLeuAspGlyMetAlaPheGlnGluAla 153
DB 358 GACCTTTTCCAGTCCGCCACACATGTCATTGTCAAG-----ACTGAACAA 402
QY 154 LeuAspProGlyProPheAspGlnGlySerProPheAlaGlnGluLeuAspAspGly 173
DB 403 ACCGATCCT-----TCCATCATGAACACATGG 429
QY 174 GlnGlnAlaSerProTrpHisProGlySerCysGlyAlaGlyAlaIleProSerProGlySer 193
DB 430 AAGAAGAAATATCTCTATGATCCAGTATGTAGACAGTACATGTTGGACAGT 489
QY 194 SerAspValSerThrAlaGlyThrGlyAlaSerArgSerSerHisSerSerAspSergly 213
DB 490 AAGACTTTTCCCGGCTCAGATCTCCATGACAACTCCAGTACTTCCAGTTGCGAGAG 549
QY 214 GlySerAspValAspLeuAspProThrAspGlyLyLeuPheProSerAspGlyPheArg 233
DB 550 TCACCTGATATG----- 561
QY 234 AspCysLyLeuGlyAspProLyHisGlyLyAspArgGlyArgProArgLyLeu 253
DB 562 -----AAAAAGAGCAAGACCACTT----- 582
QY 254 SerLyGluTrpTrpAspCysLeuGluGlyLyLeuSerLyHisAlaIleProArgGlyThr 273
DB 583 -----GTAAGTCCCAACCAAAAAGCAACCAACCAAGGACACT 621
QY 274 HisLeuTrpGluPheIleArgAspIleLeuIleHisProGluLeuAsnGluGlyLeuMet 293
DB 622 CACTTATGGAGATTCAATCCGAGCATTTCTTGAAGCCAGACAAAGAACCCAGGGCTGATC 681
QY 294 LyGTrpGluAsnArgHisGlyGlyValPheLyAspPheLeuArgSerglyAlaValAlaGln 313
DB 682 AAATGGGAAGACCGTTCGGAAGGCACTTTCAGGTTCTGTGAAGTCAGAAGCTGTGGCTCAG 741
QY 314 LeuTrpGluGlnLyAspLyAsnSerAsnMetThrTyGluLyAspSerArgAlaMet 333
DB 742 CTGTGGGGGAAAGAAATAATACATGATGATACATACGAGAAAGCTTACGCGGGCTATG 801
QY 334 ArgTyTyTrpTyLyAspArgGluLeuGluArgValAspGlyArg 348

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DB 802 AGATATTACTACAAACGAGAAATCTGGAACGTGTGATGACGA 846

RESULT 12
US-09-009-913-8
Sequence 8, Application US/09009913
Patent No. 6087485
GENERAL INFORMATION:
APPLICANT: Ays Pharmaceuticals, Inc.
TITLE OF INVENTION: Asthma Related Genes
NUMBER OF SEQUENCES: 339
CORRESPONDENCE ADDRESS:
ADDRESSER: Bozicevic & Reed, LLP
STREET: 285 Hamilton Ave, Suite 200
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,913
FILING DATE: 21-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: SEQ-4P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3231
TELEFAX: 650-327-3231
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2280 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-009-913-8

Alignment Scores:
Pred. No.: 4.31e-32      Length: 2280
Score: 422.00           Matches: 90
Percent Similarity: 45.45%      Conservative: 50
Best Local Similarity: 29.22%    Mismatches: 70
Query Match: 21.31%           Indels: 98
DB: 3                     Gaps: 5

US-08-978-217-2 (1-371) x US-09-009-913-8 (1-2280)

QY 59 TrpLeuGluGluGlnProGlnPheTrpSerLyThrGlnValLeuAspTrpIleSerTy 78
DB 206 TGGACATCAGTCCACCTCGAATCTGAGTAAAGCCCATGTGTGGAGATGGCTCCAGTTC 265
QY 79 GlnValGluYAsnLySTYrAspAlaSerAlaIleAspPheSerArgCysAspMetAsp 98
DB 266 TGGTGGACAGTACAAAGTTGAGACACCAATGATCTCTTCACTTCACTTCAATCAATCA 325
QY 99 GlyAlaThrLeuCYsAsnCysAlaLeuGluGluLeuAspGluValPheGlyProLeuGly 118
DB 326 GGCCTGACGCTGTGACAGATGACACAGAGAGGTTCTGTGAGGACGCTGCGCTGCGGC 385
QY 119 AspGlnLeuHisAlaGlnLeuArgAspLeuThrSerSerSerAspGluLeuSerTrp 138
DB 386 GAGTACCTGTACTTCAATCTCCAAACATCCGACA----- 421
QY 139 IleIleGluLeuGluLyAspGlyMetAlaPheGlnGluAlaLeuAspProGlyPro 158

```

```

Db 421 ----- 421
Qy 159 PheapngllyserProPheAlaglnluleuAaspGlyGlnGlnAlaserPro 178
Db 422 -----CAAGTTACTCTTTTAAATGACCGCTGAAGAAAGCAAGCCACATCAAGAC 475
Qy 179 TyrHisProGlyserCyGlyAlaGlyAlaProSerProGlySerSerAspValSerThr 198
Db 476 TATCGTATTCACACTGC-----TTGAANAACA 502
Qy 199 AlaGlyThrGlyAlaSerArgSerSerHisSerSerAspSerGlyGlySerAspValasp 218
Db 503 AGTGGCATC--AAAGTCAAGACTGTACAGT----- 532
Qy 219 LeuAspProThrAspGlyLysLeuPheProSerAspGlyPheArgAspCysLysLysGly 238
Db 532 ----- 532
Qy 239 AspProLysHisGlyLysArgLysArgGlyArgProArgLysLeuSerLysGlyTyrTrp 258
Db 532 ----- 532
Qy 259 AspCysLeuGlnGlyLysLysSerLysHisAlaProArgGlyThrHisLeuTyrGluPhe 278
Db 533 -----CATAGTAGAACAAAGCCCTCCAAAGTTCATCTCATGTAGGAATTT 574
Qy 279 IleArgAspIleLeuIleHisProGlnLeuAsnGlnGlyLeuMetLysTyrGlnAsnArg 298
Db 575 GTAGAGACCTGCTTCTATCTCTGAAAGAACTGTGGCATTTCTGGAATGGAAAGATGG 634
Qy 299 HisGlnGlyAlaPheLysPheLeuArgSerGlnAlaValAlaGlnLeuTyrGlnLys 318
Db 635 GAACAGAGAAATTTTCGGGTGTAAATCGAAGCCCTGGCAAGATGTGGGCAAGAC 694
Qy 319 LysLysAsnSerAsnMetThrTyrGlnLysLeuSerArgAlaMetArgTyrTyrLys 338
Db 695 AAGAAAATGACAGAAATGACGTATGAAAGTTGAGCAGAGCCCTGAGATCTACTATAA 754
Qy 339 ArgGlnIleLeuGlnArgValAspGlyArgArgLeuValTyrLysPheGlyLysAsnSer 358
Db 755 ACAGGAATTTTGGAGCGGTGGAC--CGAAGTTAGTGAATTTGAAAAAATGCA 811
Qy 359 SerGlyTyrLysGlnGlnGlnVal 366
Db 812 CACGGGTGCGAAGACAACTA 835

RESULT 13
US-09-009-913-6
; Sequence 6, Application US/09009913
; Patent No. 6087485
GENERAL INFORMATION:
; APPLICANT: Axy's Pharmaceuticals, Inc.
; TITLE OF INVENTION: Asthma Related Genes
; NUMBER OF SEQUENCES: 339
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bozicevic & Reed, LLP
; STREET: 285 Hamilton Ave, Suite 200
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94301
COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: 21-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

```

```

; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela J
; REGISTRATION NUMBER: 36,677
; REFERENCE/DOCKET NUMBER: SEQ-4P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-327-3231
; TELEFAX: 650-327-3231
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2428 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-009-913-6

Alignment Scores:
Pred. No.: 4.74e-32 Length: 2428
Score: 422.00 Matches: 90
Percent Similarity: 45.45% Conservative: 50
Best Local Similarity: 29.22% Mismatches: 70
Query Match: 21.31% Indels: 98
DB: Gaps: 5

US-08-978-217-2 (1-371) x US-09-009-913-6 (1-2428)
Qy 59 TyrLeuGlnGlnGlnProGlnPheTyrSerLysThrGlnValLeuAspTyrPheSerTyr 78
Db 354 TGACATCACTCCACCTGAAATCTGATGAAGGCGCATGTGTGGAGTGGCTCCACATTC 413
Qy 79 GlnAlaGlnLysAsnLysTyrAspAlaSerAlaIleAspPheSerArgCysAspMetAsp 98
Db 414 TGCTGCACCACTACCAAGTTGACACCAATTCATCTCTTCTGCACTTCAATCAATCACT 473
Qy 99 GlyAlaThrLeuCyAsnCysAlaLeuGlnGlnLeuArgLeuValPheGlyProLeuGly 118
Db 474 GGCTGCAGCTGTGCACAGATGACACAGAGAGATTGTCGAGCAGCTGGCTCTGCGGC 533
Qy 119 AspGlnLeuHisAlaGlnLeuArgAspLeuThrSerSerSerSerAspGlnLeuSerTyr 138
Db 534 GAGTACCTGTACTTCATCTCCACAGACATCCGCACA----- 569
Qy 139 IleIleGlnLeuLeuGlnLysAspGlyMetAlaPheGlnGlnAlaLeuAspProGlyPro 158
Db 569 ----- 569
Qy 159 PheapngllyserProPheAlaglnluleuAaspGlyGlnGlnAlaserPro 178
Db 570 -----CAAGTTACTCTTTTAAATGACCGCTGAAGAAAGCAAGCCACATCAAGAC 623
Qy 179 TyrHisProGlyserCyGlyAlaGlyAlaProSerProGlySerSerAspValSerThr 198
Db 624 TATCGTATTCACACTGC-----TTGAANAACA 650
Qy 199 AlaGlyThrGlyAlaSerArgSerSerHisSerSerAspSerGlyGlySerAspValasp 218
Db 651 AGTGGCATC--AAAGTCAAGACTGTACAGT----- 680
Qy 219 LeuAspProThrAspGlyLysLeuPheProSerAspGlyPheArgAspCysLysGly 238
Db 680 ----- 680
Qy 239 AspProLysHisGlyLysArgLysArgGlyArgProArgLysLeuSerLysGlyTyrTrp 258
Db 680 ----- 680
Qy 259 AspCysLeuGlnGlyLysLysSerLysHisAlaProArgGlyThrHisLeuTyrGluPhe 278
Db 681 -----CATAGTAGAACAAAGCCCTCCAAAGTTCATCTCATGTAGGAATTT 722
Qy 279 IleArgAspIleLeuIleHisProGlnLeuAsnGlnGlyLeuMetLysTyrGlnAsnArg 298

```

```

Db 723 GTACAGACCTCTCTTACTCTCTGAGAACTGTGGCATTCCTGAAAGGAGATAG 782
Qy 299 HlsglgllyvalPheLysPheLeuArgSerGluAlaValAlaGlnLeuTrpGlyGlnLys 318
Db 783 GAACAAGGAATTTTCGGGTGGTAAATCGAAGCCCTGGCAAAAGATGGGGAACAAAG 842
Qy 319 LysLysAsnSerAsnMetThrTyrGlnLysLeuSerArgAlaMetArgTyrTyrLys 338
Db 843 AAGAAAAATGACAGATATGATGATAAAAGTTGAGCAGAGCCCTGAGATACTACTATAA 902
Qy 339 ArgGlnLysLeuGlnArgValAspGlyArgArgLeuValTyrLysPheGlyLysAsnSer 358
Db 903 ACAGGAATTTTGAGCGGGTTGAC---CGAAGTTAGTGTACAAATTTGAAAAAATGCA 959
Qy 359 SerGlyTrpLysGlnGlnGlnVal 366
Db 960 CACGGGTGGCAGGAAGACAGCTA 983

```

## RESULT 14

```

US-09-009-913-10
Sequence 10, Application US/09009913

```

```

Parent No. 6087485

```

```

GENERAL INFORMATION:

```

```

APPLICANT: Axy's Pharmaceuticals, Inc.

```

```

TITLE OF INVENTION: Aslhma Related Genes

```

```

NUMBER OF SEQUENCES: 339

```

```

CORRESPONDENCE ADDRESS:

```

```

ADDRESSEE: Bozicevic & Reed, LLP

```

```

STREET: 285 Hamilton Ave, Suite 200

```

```

CITY: Palo Alto

```

```

STATE: CA

```

```

COUNTRY: USA

```

```

ZIP: 94301

```

```

COMPUTER READABLE FORM:

```

```

MEDIUM TYPE: Diskette

```

```

COMPUTER: IBM Compatible

```

```

OPERATING SYSTEM: DOS

```

```

SOFTWARE: FastSeq for Windows Version 2.0

```

```

CURRENT APPLICATION DATA:

```

```

APPLICATION NUMBER: US/09/009,913

```

```

FILING DATE: 21-JAN-1998

```

```

CLASSIFICATION:

```

```

PRIOR APPLICATION DATA:

```

```

APPLICATION NUMBER:

```

```

FILING DATE:

```

```

ATTORNEY/AGENT INFORMATION:

```

```

NAME: Sherwood, Pamela J

```

```

REGISTRATION NUMBER: 36,677

```

```

REFERENCE/DOCKET NUMBER: SEQ-4P

```

```

TELECOMMUNICATION INFORMATION:

```

```

TELEPHONE: 650-327-3231

```

```

TELEFAX: 650-327-3231

```

```

TELEX:

```

```

INFORMATION FOR SEQ ID NO: 10:

```

```

SEQUENCE CHARACTERISTICS:

```

```

LENGTH: 2498 base pairs

```

```

TYPE: nucleic acid

```

```

STRANDEDNESS: double

```

```

TOPOLOGY: linear

```

```

MOLECULE TYPE: cDNA

```

```

US-09-009-913-10

```

## Alignment Scores:

```

Pred. No.: 4,956-32 Length: 2498
Score: 422.00 Matches: 90
Percent Similarity: 45.45% Conservative: 50
Best Local Similarity: 29.22% Mismatches: 70
Query Match: 21.31% Indels: 98
DB: 3 Gaps: 5

```

```

US-08-978-217-2 (1-371) x US-09-009-913-10 (1-2498)

```

```

Qy 59 TrpLeuGlyGlnProGlnPheTrpSerLysThrGlnValLeuAspTrpLysSerTyr 78
Db 423 TGGACATCAGTCACCCCTGAATACGAGCTAAGCCCATGCTGGAGCTGCTCCAGTTC 482
Qy 79 GlnValGlnLysAsnLysTyrAspAlaSerAlaLeuAspPheSerArgCysAspMetAsp 98
Db 483 TGCTGCAGCCAGTACAGTATGAGACCAATTCATCTCTTCTGCACTTCAACATCTAGT 542
Qy 99 GlnAlaThrLeuCysAsnCysAlaLeuGlnGlnLeuArgLeuValPheGlyProLeuGly 118
Db 543 GGCCTGCAGCTGTGTGACATACACAGAGAGATTCCGTGAGGACGCTGCGCTGCGGC 602
Qy 119 AspGlnLeuH1sAlaGlnLeuArgAspLeuThrSerSerSerSerAspGlnLeuSerTrp 138
Db 603 GAGTACCTGTACTTCATCTCCAGAACATCCGACACA----- 638
Qy 139 IleIleGlnLeuLeuGlnLysAspGlyMetAlaPheGlnGlnAlaLeuAspProGlyPro 158
Db 638 ----- 638
Qy 159 PheAspGlnGlySerProPheAlaGlnGlnLeuLeuAspAspGlyGlnGlnAlaSerPro 178
Db 639 -----CAAGTTACTCTTTTATATGACCGCTGAAGAAAGCAAGCCACCATCAAGAC 692
Qy 179 TyrHisProGlySerCysGlyAlaGlyAlaProSerProGlySerSerAspValSerThr 198
Db 693 TATGCTGATTCCACTGC-----TTGAAAACA 719
Qy 199 AlaGlyThrGlnAlaSerArgSerSerHisSerSerAspSerGlyGlySerAspValAsp 218
Db 720 AGTGGCATC---AAAAGTCAAGACTGTCAAGT----- 749
Qy 219 LeuAspProThrAspGlyLysLeuPheProSerAspGlyPheArgAspCysLysLysGly 238
Db 749 ----- 749
Qy 239 AspProLysHisGlyLysArgLysArgGlyArgProArgLysLeuSerLysGlyTrpTrp 258
Db 749 ----- 749
Qy 259 AspCysLeuGlnGlyLysLysSerLysHisAlaProArgGlyThrHisLeuTrpGlnPhe 278
Db 750 -----CATAGTAGAACAAAGCCCTCCAAAGTTCTCATCTATGGGAATTT 791
Qy 279 IleArgAspIleLeuIleHisProGlnLeuAsnGlnGlyLeuMetLysTrpGlnAsnArg 298
Db 792 GTACAGACCTGCTCTTACTCTCTGAGAAAGATGCGCATTTCTGGAATGGGAAGATAGG 851
Qy 299 HlsglgllyvalPheLysPheLeuArgSerGluAlaValAlaGlnLeuTrpGlyGlnLys 318
Db 852 GAACAAGGAATTTTCGGGTGGTAAATCGAAGCCCTGGCAAAAGATGGGGAACAAAG 911
Qy 319 LysLysAsnSerAsnMetThrTyrGlnLysLeuSerArgAlaMetArgTyrTyrLys 338
Db 912 AAGAAAAATGACAGATATGATGATAAAAGTTGAGCAGAGCCCTGAGATACTACTATAA 971
Qy 339 ArgGlnLysLeuGlnArgValAspGlyArgArgLeuValTyrLysPheGlyLysAsnSer 358
Db 972 ACAGGAATTTTGAGCGGGTTGAC---CGAAGTTAGTGTACAAATTTGAAAAAATGCA 1028
Qy 359 SerGlyTrpLysGlnGlnGlnVal 366
Db 1029 CACGGGTGGCAGGAAGACAGCTA 1052

```

## RESULT 15

```

US-08-368-281-1
Sequence 1, Application US/08368281
Parent No. 5721113
GENERAL INFORMATION:
APPLICANT: Libermann, Towia A
APPLICANT: Oetegen, Joerg P
APPLICANT: Kunisch, Charles A
TITLE OF INVENTION: NERF Genes

```

NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: SmithKline Beecham Corporation  
 STREET: 709 Swedeland Road  
 CITY: King of Prussia  
 STATE: Pennsylvania  
 COUNTRY: USA  
 ZIP: 19406  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/368,281  
 FILING DATE:  
 CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Baumeister, Kirk  
 REGISTRATION NUMBER: 33,833  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 610-270-5096  
 TELEFAX: 610-270-5090  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2975 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 US-08-368-281-1

## Alignment Scores:

Pred. No.: 1,41e-14 Length: 2975  
 Score: 246.50 Matches: 74  
 Percent Similarity: 40.43% Conservative: 40  
 Best Local Similarity: 26.24% Mismatches: 78  
 Query Match: 12.45% Indels: 90  
 DB: 1 Gaps: 9

US-08-978-217-2 (1-371) x US-08-368-281-1 (1-2975)

QY 139 ILeIleGluleuLeuGluYAspGlyMeAlaPheGInGluAlaLeuAspProGlyPro 158  
 Db 1 GTGGTAGTGTCGTCGCGACGCGGCGGTCCGCGCGGCGGTCCGCTCCCTCC 60  
 QY 159 PheAspGInGlySerProPheAlaGInGluLeuAspAspGlyGInGluAlaSerPro 178  
 Db 61 CTG-----CCGCGCTGCTCAGCGGTGAAGTGAAGCAGAGCTCCAGCCC 111  
 QY 179 -----TyrHisProGlySerCysGlyAla 186  
 Db 112 CGGATTAACATGCGCAGCTTCTGCATGAGGACCCACGAACA-----GCT 159  
 QY 187 G1yAlaProSerProGlySerSerAspValSerThr----- 198  
 Db 160 GGATCTGCTCATCCGCGCCGCGGAAGCATCACTTCACAGCAGTAATGACACTGTACAGA 219  
 QY 199 -----AlaGlyThrGlyAlaSer----- 204  
 Db 220 TAAGACAATTGAAGCTGTAAGCCCTGTCATATGGAATCTCTACCTTGAGGGA 279  
 QY 205 -----ArgSerSerHisSerSerAsp 211  
 Db 280 TTCAAGAGTCCTGAATTCATCTGCTATGAGGCCAGATGTCAATTAACGAATACTGT 339  
 QY 212 SerGlyGly-SerAspValAspLeuAspProThrAspGlyLysLeuPheProSer----- 229  
 Db 340 AGTGAAGTGTCACTGAAGAGTCTGAAGCCATGATACCTCTCTATTCACATCAAC 399  
 QY 230 -AspGlyPheArgAspCysLysLys----- 237  
 Db 400 AGATAGCCATGAACCAATGAAGAAAAAGATTGGCCGTAACCAAGACCAGCAATC 459

QY 238 -----GlyAspProLysHisGlyLysArgLysArgGlyArgProArgLysLe 253  
 Db 460 ACCAATTTCCAAATGGGCTCTCTGAGTTAGGTATTAAGAAACCAAGA----- 508  
 QY 253 uSerLysGluTyr-TTrrAspCysLeuGluGlyLysSerLysHisAlaProArgGlyTh 273  
 Db 509 -----GAAGGAAAAAGAAACACA-----AC 528  
 QY 273 rHisLeuTrrGluPheIleArgAspIleLeuIleHisProGluLeuAsnGluGlyLeuMe 293  
 Db 529 CTATTTGTGGAGTTCTTTTATGATCTACTTCAAGATAAAAATACTTGTCCAGGTATAT 588  
 QY 293 LysTrrGluAsnArgHisGluGlyValPheLysPheLeuArgSerGluAlaValAlaG1 313  
 Db 589 TAAATGACTCAGAGAGAAAAAGGCATATTCAAGCTGTGATTCAAAGGCTGTCTAA 648  
 QY 313 nLeuTrrGlyGlnLysLysLysSerAsnMetThrTyrGluLysLeuSerArgAlaMe 333  
 Db 649 GCTTTGGGAAAGCATTAAGAACAAACCAACATGAACTATGAAACCATGGAGAGCTTT 708  
 QY 333 LArgTyrTrrLysArgGluIleLeuGluArgValAspGlyValArgPheLeuValTyrLys 353  
 Db 709 GAGTACTACTTACCAAGGGAATTTTTCGAAAGGTTGAAGACAGAGCTTGTATATCA 768  
 QY 353 sPhe 354  
 Db 769 GTTC 772

Search completed: March 15, 2003, 23:32:40  
 Job time: 94.0238 secs

